

Figure 1

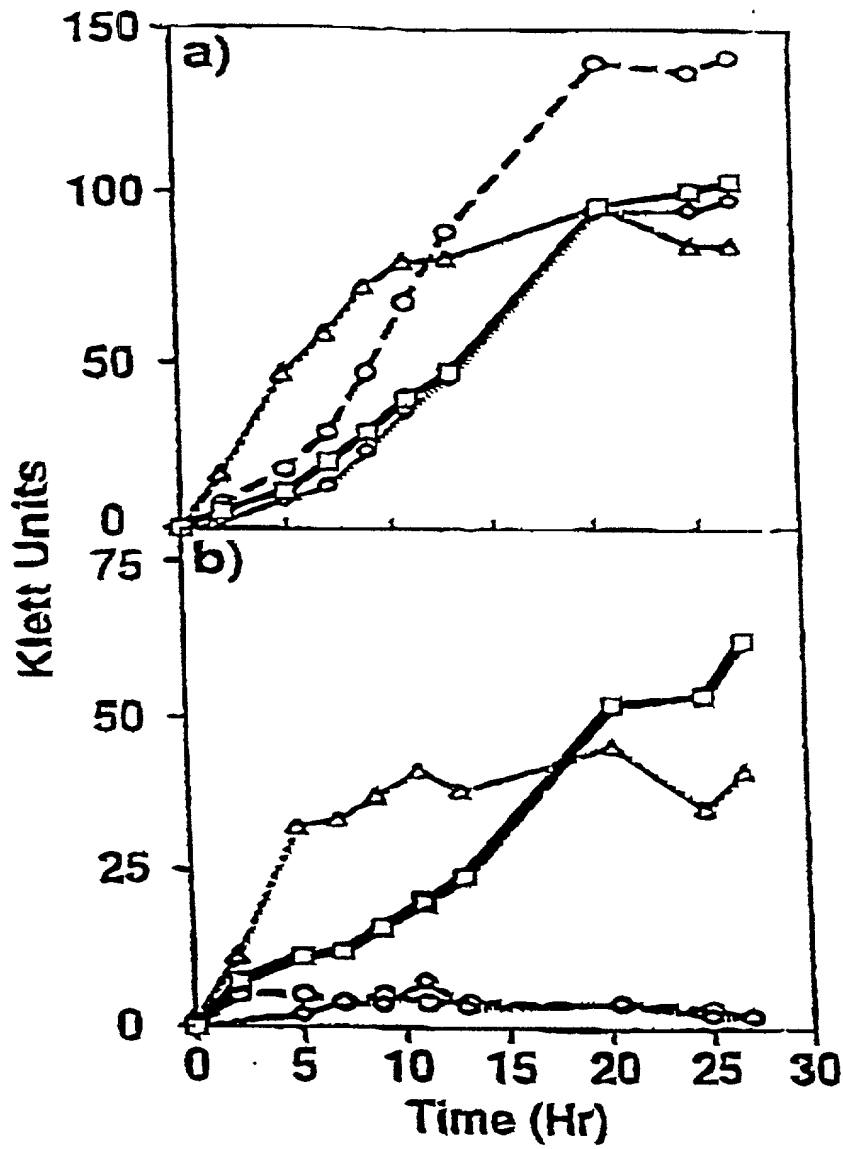
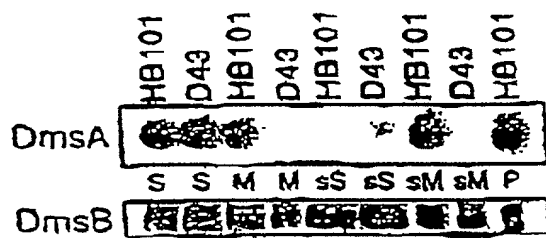


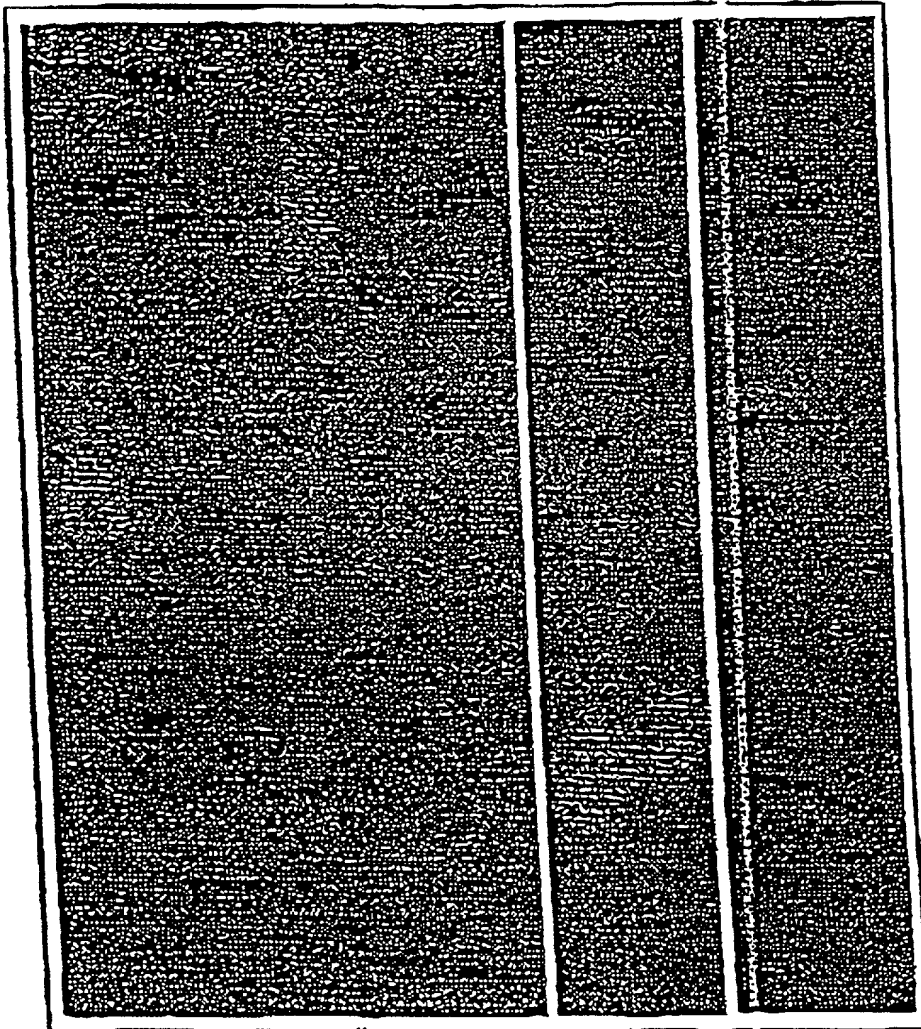
Figure 2



2

Figure 3

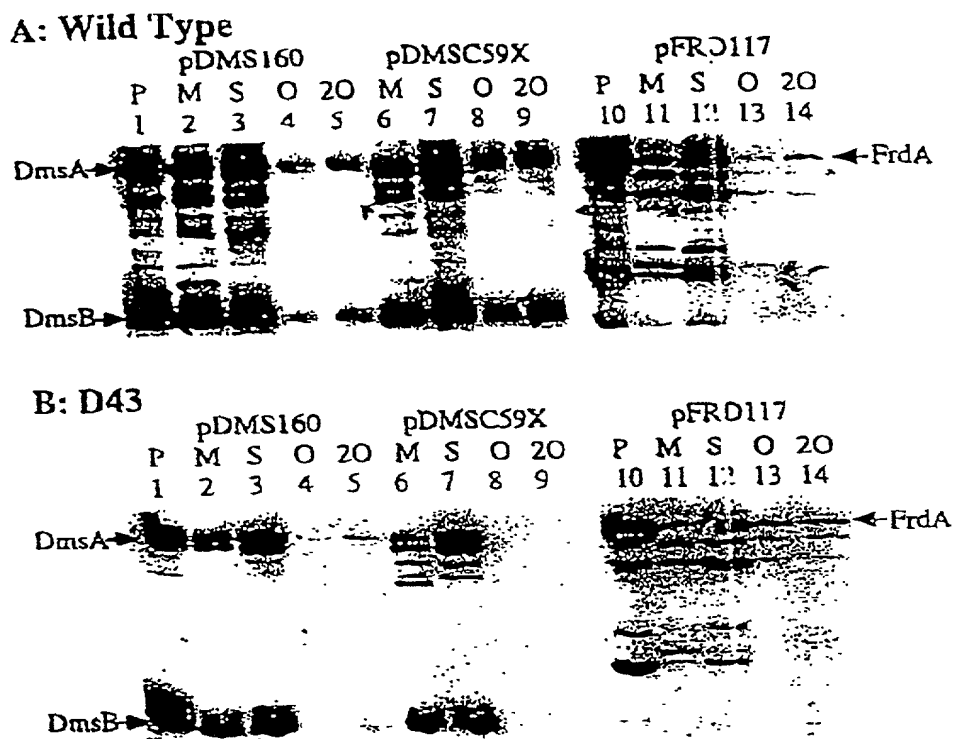
a) b) c)
1 2 3 4 5 6 1 2 1 2



209T40" FZTE200T

202311.041602

Figure 4



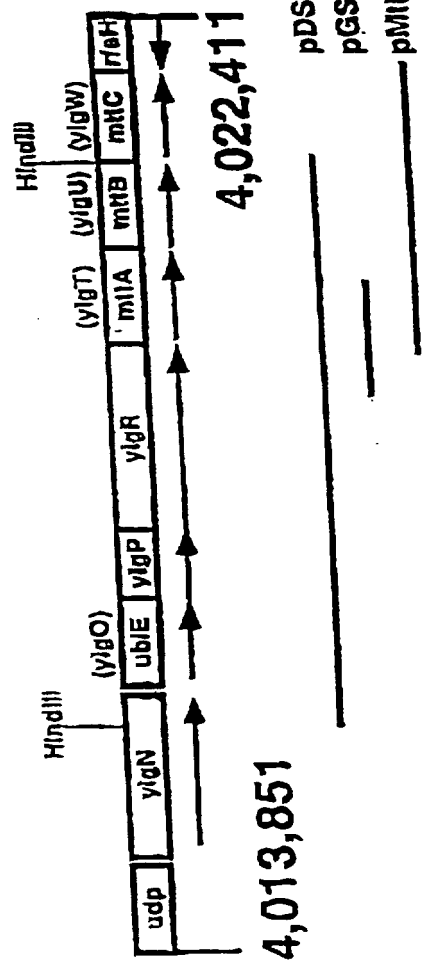


Figure 5

Figure 6

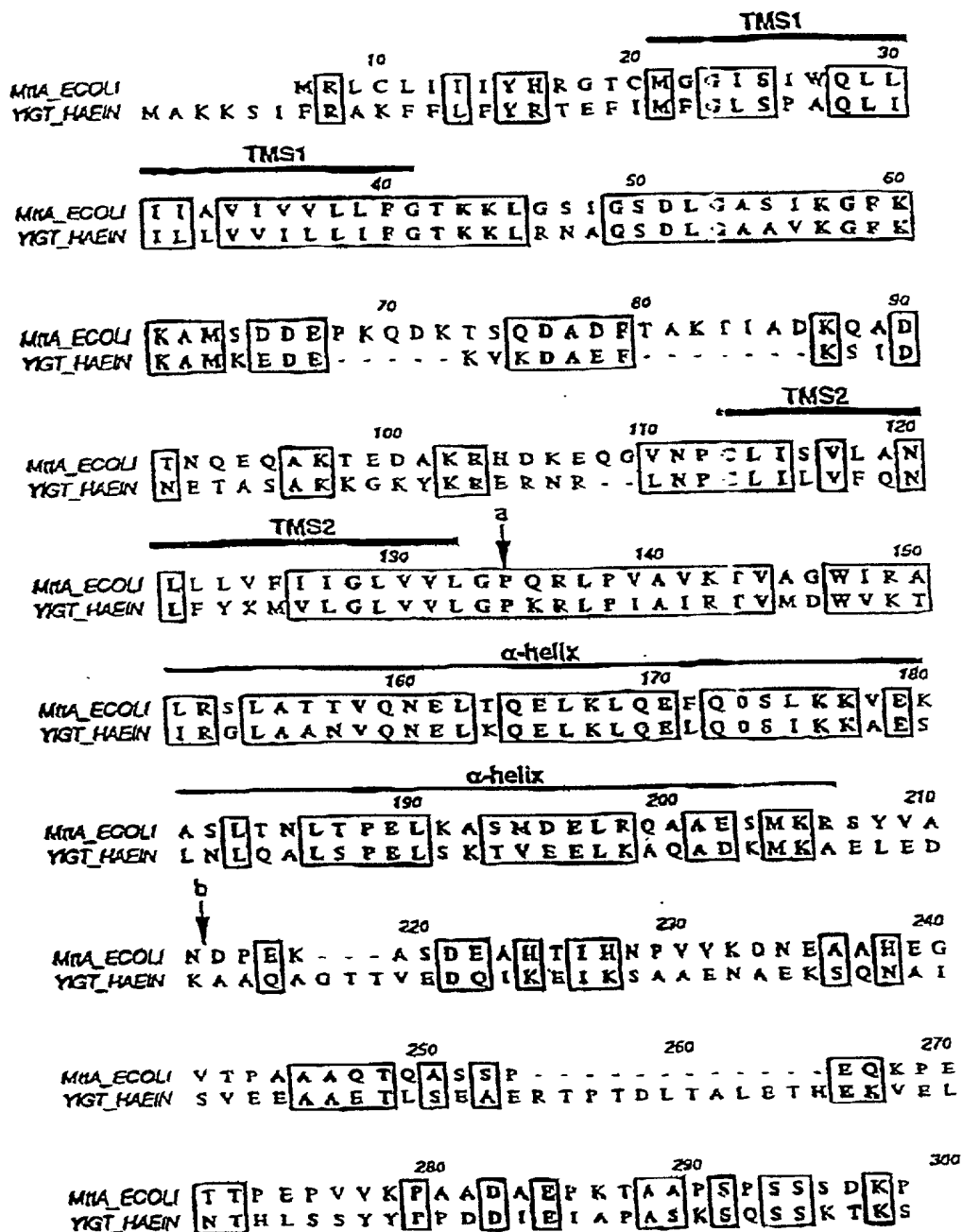


Figure 7(A)

Figure 7(B)

GGAACAGGCTAAACAGAGACGGGAAGCGCCACGATAAGAGCAGGTGAATCCGTGTTT
E Q A K T E D A K R H D K E Q V N F C L>
ORF RF(3) >

5960 5970 5980 5990 6000 6010
GATATCCGTTTATAGCGAAGTTCCTATTGGTGTATCATCGGGCTCGTCTTCGGGGC
I S V L A H L L L V F I I G L V V L C F>
ORF RF(3) >

6020 6030 6040 6050 6060 6070
GCACCACTGCTCTGCGCGTAANACCGTACCGCGCTGGATTGCGCGGTTCGGTCACT
Q R L P V A V K T V A G W I R A L R S L>
ORF RF(3) >

6080 6090 6100 6110 6120 6130
GGCGACACGGTGCAGAACGAACTGACCCAGGACTTAAACTCCAGGAGTTTCAGGACAG
A T T V Q N E L T Q E L K L Q E F Q D S>
ORF RF(3) >

6140 6150 6160 6170 6180 6190
TCIGAAAAGGTTGAAAAGCGAGCGCTCACTAACCTGACCGCCGAACTGAAAGCGTCGAT
L K K V E K A S L T N L T P E L K A S M>
ORF RF(3) >

6200 6210 6220 6230 6240 6250
GGATCAACTACGCCAGGTGCGCGAGTGCATGACCGCTTCCTACGTTGCAAAACGATCCTGA
D E L R Q A A E S H K R S Y V A N D P E>
ORF RF(3) >

6260 6270 6280 6290 6300 6310
AAAGGCGAGCGAIGAGGCGCACACCATCCATAACCGGTGCTGAAAGATATGAAGCTCC
K A S D E A H T I H N F V V K D N E A A>
ORF RF(3) >

6320 6330 6340 6350 6360 6370
GCATGAGGCGCTAAAGCTCTCCCGTGCACAAAGCAGGCGAGTTGCGCGGAACAGAGCC
H E G V T P A A A Q T Q A S S P E Q K P>
ORF RF(3) >

6380 6390 6400 6410 6420 6430
AGAAACCAAGGCGAGCGCGCTGGTAAACCTGCTCCGAGCGCTGAACCGAANACCGCTGC
E T T P E F V V K T A A D A E P K T A A>
ORF RF(3) >

6440 6450 6460 6470 6480 6490
ACCTTCCCGCTCGTGGAGTGATAAACCGTAACATGCTGTGTAGAGATACTCAACCGTT
M S V E D T Q E L>
ORF RF(2) >

P S P S S S D K P>
ORF RF(3) >

6500 6510 6520 6530 6540 6550
ATCACGCATCTGATTGAGCTCGGTAGCGTCTGCTGAAGTGCATTATCGCGGTGATCGTG
I T E L I E L R K R L L W C I I A V I V>
ORF RF(2) >

6560 6570 6580 6590 6600 6610
ATATTCTGTGTCTGCTGATTTCCCAATGACATCTATCACCTGGTATCCGGCGCATTC

10023171.041602

Figure 7(D)

```

1280      7290      7300      7310      7320      7330
XGGAGTACAGGAATGTTGATATCGCGGTTAATTTCACCAGTTCGCAATTTCGGAAAGACC
H E Y R K F D I G V N L T S S Q F A K D>
ORF RF(1)

7340      7350      7360      7370      7380      7390
CTCATGATGTTGTAGCGTCCGCTTTTCACCGGGGAGTTAATCGGCTACTCATCACCGGCA
R D O V V A C A F D A G V N G L L I T C>
ORF RF(1)

7400      7410      7420      7430      7440      7450
CTAACCTCGGTCGAAGCCAGCAGCGCCCAAAAGCTGGCGGTCAGTATTCCGTCCTGTTGGT
T N L R E S Q Q A Q K L A R Q Y S S C W>
ORF RF(1)

7460      7470      7480      7490      7500      7510
CNAAGCGCGGCGTACATCCTCAGCAGCAGCCAGTGGCAAGCTGGCACTGAAGAAGCGA
S T A G V R P R D S S Q W Q A A T E E A>
ORF RF(1)

7520      7530      7540      7550      7560      7570
TTATTAGCTGGCCCGCCAGCCAGAACTGGTGGCGATGGTGAATGTGGTCTCGACTTTA
I I E L A A Q P E V V A I G E C G L D F>
ORF RF(1)

7580      7590      7600      7610      7620      7630
ACCGCAACTTTTCGACCGCGGAGAGCAGGAACGCGCTTTTGTGGCCAGCTACGCATTG
N R H F S T P E E Q E R A F V A Q L R I>
ORF RF(1)

7640      7650      7660      7670      7680      7690
CCGCAGATTAAACATGCCGGTATTATGCACTGTCGGGATGCCCAAGAGCGGTTTATGA
A A D L N M P V F H H C R D A H E R F H>
ORF RF(1)

7700      7710      7720      7730      7740      7750
CATTCCGGAGCCCGTGGCTGGATAACTGCCTGCTGGCTTCTTCATTGCTTTACCGGCA
I L L E E M L D K L P G A V L E C F T G>
ORF RF(1)

7760      7770      7780      7790      7800      7810
CAOCCGAAGAGATGCAGCGCTCCGTCGGCATGGAATTTATAICGGCAITACCGGTTCGG
T R E E M Q A C V A B G I Y I G I T G W>
ORF RF(1)

7820      7830      7840      7850      7860      7870
TTTCCGATGAACGACCGGACTGGAGCTGCGGCACTTTTGGCGTIGATTCCCGCGGAAA
V C D E R R G L E L R E L L P L I P A E>
ORF RF(1)

7880      7890      7900      7910      7920      7930
AATTACTGATCGAATGATGCGGCTATCTGCTCCCTCGGATCTCAGGCAAGGCAT
K L L I E T D A P T L L P R D L T P K E>
ORF RF(1)

7940      7950      7960      7970      7980      7990
CATCCCGGCGCAACGAGCCAGCCATCTGCCCCATATTTTGCACGCTATTCGGCACTGGC

```

Figure 7(E)

S S R R N E P A K L P H I L Q R I A H W>
ORF RF(11) >

8000 8010 8020 8030 8040 8050
GTGAGAGATGCCGATGGCTGGCTGCCACCGGATGCTAATGTCAAAACACTGTTC
K G E D A A W L A A T T D A N V K T L F>
ORF RF(11) >

8060 8070 8080 8090 8100 8110
GGATTGGCTTTAGAGTTTGGGAACTGGTATTCTTCACACTGTGCTTAATCTCTTTAT
C I A F>

8120 8130 8140 8150 8160 8170
TAATAAGATTAAAGCAATAGCATGGAGCGGCTCACCATCGGGTTCGGTGAAAATGGCCT

8180 8190 8200 8210 8220 8230
GAAAGCCTTCCAACGGGCTTTCGGTAATAATCACCCTATCAACCGGATAAGGGGTTCGGC

8240 8250 8260 8270 8280 8290
GATCGACAATGTCTTTCGGTTTATATACCGATAGCTGATGAATAACCGCGGATGGGACTA

8300 8310 8320 8330 8340 8350
TCCCTGGCGACGGGCAAGCGGACGAACTGGCTGACACCGCGGCTGGCTGTATAGTCG

8360 8370 8380 8390 8400 8410
TGGTATCAATCACTTCTGGGTCAAATTCACCAACAGGTAGTTGGCGAACATGGGTCAC

8420 8430 8440 8450 8460 8470
TGACTGCACTACGTTTCCACCGCAGGATTTTCCAGGGTGATCATCGGTGGCAGGCAAT

8480 8490 8500 8510 8520 8530
TCACAGCTGTCTTCCAGGTGTTCCTGGGCACGTTGAAGTTGCCCGGCTTCGAGTACA

8540 8550 8560 8570 8580 8590
GTAAATACCAAGATTGCATAATGACTCTTATCCCTTTAATCGGCGCCAGGATAGCAAA

8600 8610 8620 8630 8640 8650
AGCTTACCTAAGCTAATTAATATTCGGCGGTTTCGGTATACGCTCAGAGTTCAGCTA

8660 8670 8680 8690 8700 8710
ATTTAACTAATTTACAGCATCCCAAGATCAAGCGCGTATAATCGCCGAGATTAGAGG

8720 8730 8740 8750 8760 8770
CTACAACTGACCCCATCAATAATAACGATTTACGGGACTTCTTCACCTGCTTGAACGC

8780 8790 8800 8810 8820 8830
AGGGTGAGCTAAACGATACCGCTCCGGTGCATCCGATCTCGAATCAGTGAATTC

8840 8850 8860 8870 8880 8890
CTGACCGGCTTTCCCTCCCGCTCCCGCTCCGCTGTTGTTCCAAACCTTAACGCTACT

8900 8910 8920 8930 8940 8950
CAATGCCGCTCTGTGCAACCTGTTCGTACGCCAAACCGCGTCCGATGGGCAATGGGGC

8960 8970 8980 8990 9000
AGGAAGATCTTTCGGCGCTGGGTGAAGTTCGTAATTAATG

1002471.044602

11

Figure 8(A)

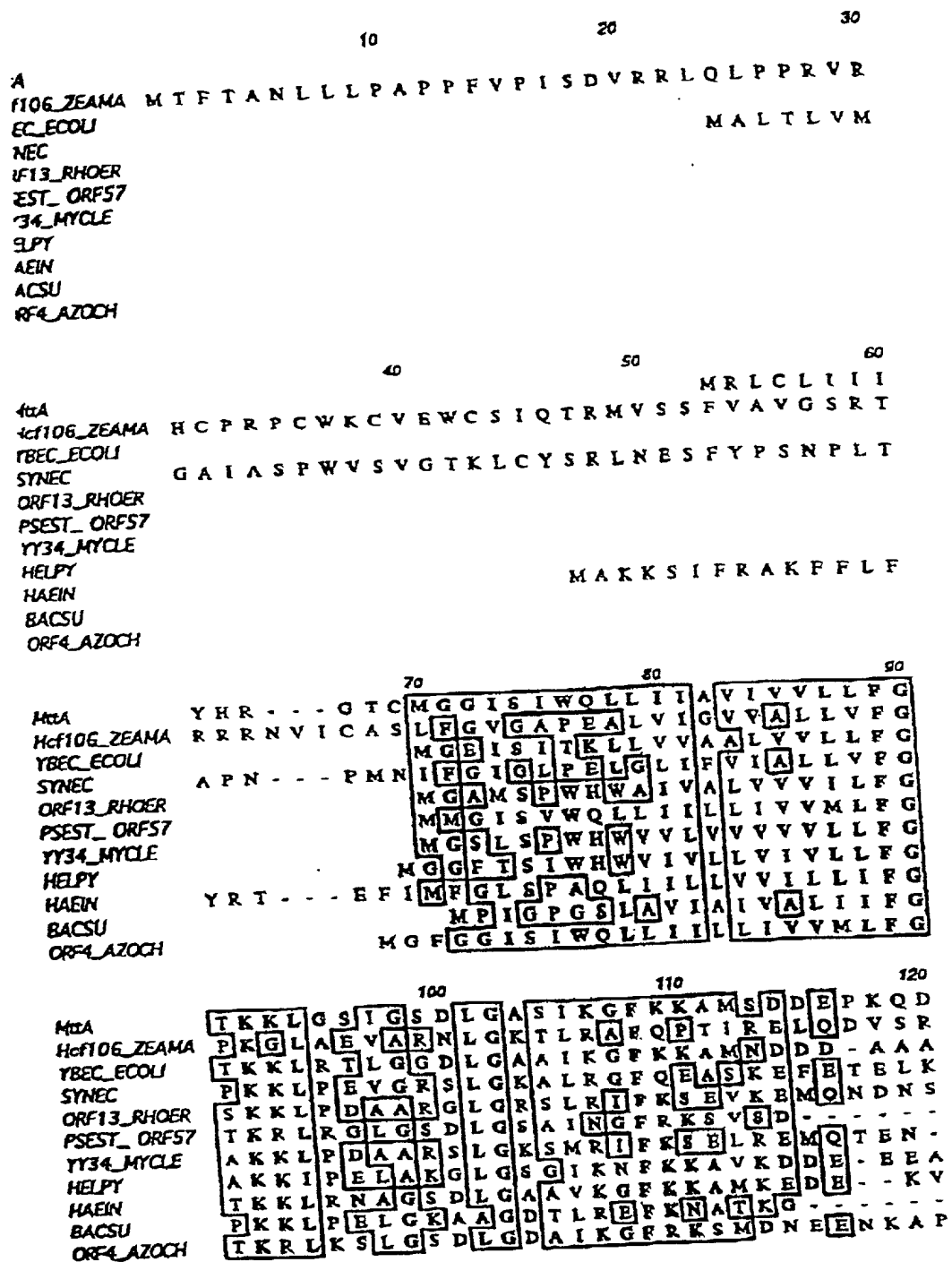


Figure 8(B)

		130	140	150																										
MTA	KTSQD-A--DFTAKTI	A	D	K	Q	A	D	T	N	Q	E	Q	A	K																
Hcf106_ZEAMA	EFRSTLEREIGIDEVSQ	S	T	K	Y	R	P	T	M	N	N	N	Q																	
YBEC_ECOLI	KKGAD-V--DLQA	E	K	L	S	H	K	E																						
SYNEC	REAQNLE--KSVQIKAE	L	E	B	E	S	K	T	P	E	S	S	S	S																
ORF13_RHOER	TPAPTAQ--SAPP	P	Q	S	A	P	A	E	L	P	V	A	D	T	T	T	A													
PSEST_ORF57	-----																													
YY34_MYCLE	-----Q--AQASALE	T	P	M	Q	N	P	T	V	V	Q	S	Q	R																
HELPI	KNBP--K--TLDAQAT	Q	T	K	V	H	E	S	S	E	I	K	S	K																
HAEN	KDAEF-K--SIDNETA	S	A	K	K	G	K	Y	K	R	B	R	N	R																
BACSU	-----																													
ORF4_AZOCH	PVEEQ-K--GQDHRG	P	G	P	Q	G	R	G	T	G	Q	E	R	L	S															
		160	170	180																										
MTA	TEDAKRHDKEQG	V	N	P	C	L	I	S	V	L	A	N	L	L	V	F	I	I												
Hcf106_ZEAMA	Q-----																													
YBEC_ECOLI	-----																													
SYNEC	-----																													
ORF13_RHOER	P-----																													
PSEST_ORF57	-----																													
YY34_MYCLE	-----																													
HELPI	-----																													
HAEN	-----																													
BACSU	-----																													
ORF4_AZOCH	MFDIG-----																													
		190	200	210																										
MTA	GLVVLGPFQRLP	V	A	V	K	T	V	A	G	W	I	R	A	L	R	S	L	A	T	T										
Hcf106_ZEAMA	-----													P	A	A	D	P	N	V	K	P	E	R	A	P				
YBEC_ECOLI	-----																													
SYNEC	-----																													
ORF13_RHOER	-----																													
PSEST_ORF57	-----																													
YY34_MYCLE	-----																													
HELPI	-----																													
HAEN	-----																													
BACSU	-----																													
ORF4_AZOCH	A	L	L	V	L	G	P	E	R	L	P	V	A	A	R	M	A	G	L	W	I	G	R	L	K	R	S	P	N	T
		220	230	240																										
MTA	V	Q	N	E	L	T	Q	B	L	K	L	Q	E	F	Q	D	S	L	K	K	V	H	K	A	S	L	T	N	L	T
Hcf106_ZEAMA	Y	T	S	E	E	L	M	K	V	T	E	B	Q	I	A	A	S	A	A	A	A	W	N	P	Q	Q	R	A	T	S
YBEC_ECOLI	-----																													
SYNEC	-----																													
ORF13_RHOER	-----																													
PSEST_ORF57	-----																													
YY34_MYCLE	-----																													
HELPI	-----																													

Figure 8(C)

AEN VFQNLFY
 ACSU
 RF4_AZOCH LKT[E]VEREIGADEIRR - - -QLHNBRILBLE

250 260 270
 MZA PELKASMDLRQA AESMKRSYVANDPEKAS
 HcF106_ZEAMA QQQEEAPTTFR - SEDAPTSGGSSGPAAAPAR
 YBEC_ECOLI
 SYNEC
 ORF13_RHOER
 PSEST_ORF57
 YY34_MYCLE
 HELPY
 HAEIN
 BACSU
 ORF4_AZOCH REMKQSLQPPAPSAPDETAASFAATPPQPAS

280 290 300
 MZA DEAH TIHNPVVKDNEAAHEGVTPAAAQTQA
 HcF106_ZEAMA AESDSDPNQVNKSQKAEGER
 YBEC_ECOLI
 SYNEC
 ORF13_RHOER
 PSEST_ORF57
 YY34_MYCLE
 HELPY
 HAEIN
 BACSU
 ORF4_AZOCH PAAHSDKTPSP

310 320 330
 MZA SSPEQKPETTPEPVVKPAADAEKTAAPSP
 HcF106_ZEAMA
 YBEC_ECOLI
 SYNEC
 ORF13_RHOER
 PSEST_ORF57
 YY34_MYCLE
 HELPY
 HAEIN
 BACSU
 ORF4_AZOCH

340 350 360
 MZA SSSDKP
 HcF106_ZEAMA
 YBEC_ECOLI
 SYNEC
 ORF13_RHOER
 PSEST_ORF57
 YY34_MYCLE
 HELPY

Figure 9

4ttB_ECOLI	I T H L I E L R K R L L N C I I A V I V I - F L C L V Y F A	38
YC43_PORPU	T B H L E E L R Q R T V F V F I F F L L A - A T I S F T Q I	58
YM16_MARPO	K T I L E E V R I R V F W I L I C F S F T - W F T C Y W F S	34
ARATH	B T I L G E V R I R S V R I L I G I G L T - W F T C Y W F S	43
Ymf16_RECAM	L T H L Y E I R L K I I Y L L Y S I F L T - C F C S Y Q Y K	36
Y194_SYNY3	F D H L D E L R T R I F L S L G A V L V G - V V A C F I F V	58
YY33_MYCTU	V D H L T E L R T R L L I S L A A I L V T T I F G F V W Y S	57
HELPY	- - H L Q E L R K R L M V S V G T I L V A - F L G C F H F W	34
TigU_HAEIN	I T H L V E L R N R L L R C V I C V V L V - F V A L V Y F S	39
YcbT_BACSU	L E H I A E L R K R L L I V A L A F V V F - F I A G F F I A	40
YH25_AZOCH	V A H L T E L R S R L L R S V A A V L L I - F A A L F Y F A	32
ARCFU	I A L I I V I V V S S L F F T F G A N I V V C K I I G D L F P	49
MttB_ECOLI	T D V A S P F F T P I K L T F M V S L I L S A P V I L Y Q V	91
YC43_PORPU	L A P G E Y F F S S I K I A I Y C G I V A T T P F G V Y Q V	106
YM16_MARPO	T Q L T E A L S T Y V T T S L I S C F Y F L F P F L S Y Q I	87
ARATH	T Q L T E A F S T F V A T S S I A C S Y P V R P L I S Y Q I	95
Ymf16_RECAM	T D L I E A F I T Y I K L S I I V G T Y L S Y P I F L Y Q I	83
Y194_SYNY3	L S P G E F F F V S V K V A G Y S O I L V M S P F I L Y Q I	106
YY33_MYCTU	T A P F D Q R M L R L K V G M A A G I V L A C P V W F Y Q L	125
HELPY	L S P I E G V M V A V K I S F S A A I V I S M P I I F W Q L	81
TigU_HAEIN	T N I Q T P F F I P I K L T A I V A I F I S V P Y L L Y Q I	92
YcbT_BACSU	F N L T D P L Y V F M Q F A F I I G I V L T S F V I L Y Q L	90
YH25_AZOCH	T G V A S P E L A P F K L T L M I S L F L A M P V L H Q V	85
ARCFU	L T P L E G L L L Y L K I S L A V G I A A A L P Y I F H L V	139
MttB_ECOLI	W A F I A P - - - A L Y K H E R R L V Y P C L L V S S S L L F	118
YC43_PORPU	I L Y I L P - - - G L T N K E R K V I L P I L I G S I V L F	133
YM16_MARPO	W C F L M P - - - S C Y E E Q R K K Y N K L F Y L S G F C F	114
ARATH	W C F L I F - - - S C Y G E Q R T K Y N R F F Y L S G F C F	122
Ymf16_RECAM	W S F L I P - - - G F P L Y E K K L F R L L C L T S I F L Y	110
Y194_SYNY3	I Q F V L P - - - G L T R R E R R L L G P V V L G S S V L F	133
YY33_MYCTU	W A F I T P - - - G L Y Q K E R R F A V A F V I P A A V L F	152
HELPY	W L F I A P - - - G L Y K N E K K V I L P F V F F G S G M F	108
TigU_HAEIN	W A F I A P - - - A L Y Q H E K R M I Y P L L P S S T I L F	119
YcbT_BACSU	W A F V S P - - - G L Y E K E R K V T L S Y I P V S I L L F	117
YH25_AZOCH	W G F I A P - - - G L Y Q H E K R I A M P L M A S S V L L F	112
ARCFU	L T A L R E R G V I T P S F R K T S A F K Y G M A A I F L F	169
MttB_ECOLI	E G V Q V S T D I A S Y L S F V M A L F M A F G V S F E V P	172
YC43_PORPU	D I V E P L W S F E Q Y F D F I L L L L F S T G L A R E I P	187
YM16_MARPO	L I I K L Q P K I F D Y I M L T V R I L F I S S I C S Q V P	173
Arab thal mito	L M I K L Q P K I Y D Y I M L T V R I S F I S S V C S Q V P	181
Ymf16_RECAM	P T I E L Q A K I H B Y L I L N T K L I F S L S I C F Q L P	170
Y194_SYNY3	D V V E Q L W S I D K Y F E F V L L L M F S T G L A R Q I P	187
YY33_MYCTU	D V Q V T A L S G D R Y F G F L L N L L V V F G V S F E F P	206
HELPY	D V F A A N I S A S S Y V S F F T R L I L G F G V A F E L P	162
TigU_HAEIN	E G V T I A T D I S S Y L D F A L A L F L A F G V C F E V P	173
YcbT_BACSU	L N V N Q V I G I N E Y F H F L L Q L T I F F G L L F Q M P	171
YH25_AZOCH	E G Y A M M T D I G Q Y L D F V L T L E P A F G V A F E V P	160
ARCFU	Q G A I P L Y S L S E F V N F V A L M L V L F G I V F E L P	222

Figure 10

TC	TEEA	I	I	E	L	A	A	Q	-	-	P	E	V	V	A	I	G	E	C	G	L	D	F	N	R	N	F	104		
YH_ECOLI	DVED	L	R	K	L	A	A	E	-	-	E	Q	V	V	A	L	G	E	T	G	L	D	Y	Y	T	P	101			
YH_ECOLI	SLEQ	L	Q	Q	A	L	B	R	R	P	A	K	V	V	A	V	G	E	I	G	L	D	L	F	G	D	106			
YH	LIGE	V	V	S	Q	I	B	S	N	I	D	L	I	V	A	V	G	E	T	Q	M	D	F	H	H	T	107			
Y09_MYCPN	AQAT	L	K	K	L	V	S	T	H	R	S	F	I	S	C	I	G	E	Y	G	F	D	Y	H	Y	T	105			
YH_Mycu	ARAB	L	B	R	L	V	A	H	-	-	P	R	V	V	A	V	G	E	T	G	I	D	M	Y	W	P	102			
ELPY	DES	L	F	E	K	F	V	G	H	-	-	Q	K	C	V	A	I	G	E	C	G	L	D	Y	Y	R	98			
YH_HAEIN	DAER	L	L	R	L	A	Q	D	-	-	P	K	V	I	A	I	G	E	I	G	L	D	Y	Y	Y	S	104			
YABD_BACSU	DLAW	I	K	E	L	S	A	H	-	-	E	K	V	V	A	I	G	E	M	G	L	D	Y	H	W	D	101			
CHPO	-	E	A	L	A	N	K	G	K	A	S	-	G	K	V	V	A	F	G	E	F	G	L	D	Y	D	R	L	H	79
AEEL	HIS	K	M	E	Q	F	F	V	E	H	E	R	D	I	I	C	V	G	E	C	G	L	D	H	T	I	S	Q	211	
Y218_HUMAN	QERN	L	L	Q	A	L	R	H	-	-	P	K	A	V	A	F	G	E	M	G	L	D	Y	S	Y	K	C	602		

MCC	HCRDA	H	E	R	F	M	T	L	L	E	P	W	L	D	K	L	P	G	-	A	V	L	H	C	F	T	G	T	162		
YCFH_ECOLI	HTRDA	R	A	D	T	L	A	I	L	R	E	E	K	V	T	D	C	G	-	G	V	L	H	C	F	T	B	D	160		
YJNV_ECOLI	HSR	R	T	H	D	K	L	A	M	H	L	K	R	H	D	L	P	R	T	G	-	V	V	H	G	F	S	G	S	162	
METTH	HARD	A	E	E	R	A	L	B	T	V	L	E	Y	R	V	P	E	V	-	-	I	F	H	C	Y	G	G	S	164		
Y009_MYCPN	HVRD	V	H	B	R	I	Y	E	V	L	K	R	-	L	K	P	K	Q	P	-	V	V	F	H	C	F	S	E	D	161	
YCFH_Mycu	HNR	Q	A	D	R	D	V	L	D	V	L	R	A	B	G	A	P	D	T	-	V	I	L	H	C	F	S	S	D	163	
HELPY	HIRE	A	S	F	D	S	L	N	L	L	K	N	-	Y	P	K	A	F	-	G	V	L	H	C	F	N	A	D	159		
YCFH_HAEIN	HTR	S	A	G	D	D	T	I	A	M	L	R	Q	H	R	A	E	K	C	G	-	G	V	I	H	C	F	T	B	T	161
YABD_BACSU	HNR	D	A	T	E	D	V	V	T	I	L	K	E	G	A	B	A	V	G	-	G	I	M	H	C	F	T	G	S	158	
SCHPO	HSR	N	A	E	N	D	F	F	A	I	L	E	K	Y	L	P	E	L	P	K	K	G	V	V	H	S	F	T	G	S	138
CAEEL	HSR	S	A	A	R	T	I	E	I	L	E	C	H	V	A	P	D	Q	-	V	V	L	H	A	F	D	G	T	282		
Y218_HUMAN	HCRE	A	D	E	D	L	L	B	I	M	K	K	F	V	P	P	D	Y	K	-	I	H	R	H	C	F	T	G	S	660	

MCC	ERR	G	L	B	L	R	E	L	L	P	L	I	P	A	E	K	L	L	I	E	T	D	A	P	Y	L	L	P	213			
YCFH_ECOLI	RN	-	A	B	Q	L	R	D	A	A	R	Y	V	P	L	D	R	L	L	V	E	T	D	S	P	Y	L	A	P	209		
YJNV_ECOLI	PR	-	A	S	K	T	R	D	V	I	A	K	L	P	L	A	S	L	L	L	E	T	D	A	P	D	M	F	L	213		
METTH	S	-	-	-	E	H	H	M	E	L	V	R	A	I	P	L	E	G	M	L	T	E	T	D	S	P	Y	L	S	212		
Y009_MYCPN	KN	-	A	K	N	L	Q	A	A	L	S	V	I	P	T	E	L	L	S	E	T	D	S	P	Y	L	A	P	217			
YCFH_Mycu	RT	-	A	R	E	L	R	E	A	V	P	L	M	F	V	E	Q	L	L	V	E	T	D	A	P	Y	L	T	P	214		
HELPY	KN	-	A	K	R	L	V	B	I	L	P	K	I	P	K	N	R	L	L	L	E	T	D	S	P	Y	L	T	P	208		
YCFH_HAEIN	KN	-	A	E	A	I	R	E	V	I	R	Y	V	P	M	E	R	L	L	V	E	T	D	S	P	Y	L	A	P	212		
YABD_BACSU	KN	-	A	K	K	P	K	E	V	V	K	E	I	P	N	D	R	L	L	I	E	T	D	C	P	F	L	T	P	209		
SCHPO	T	-	-	-	E	E	N	L	E	V	V	R	A	I	P	L	E	K	M	L	L	E	T	D	A	P	W	C	E	V	187	
CAEEL	S	-	-	-	E	E	T	T	Q	L	I	B	S	I	P	L	S	Q	L	L	L	E	T	D	S	P	A	L	G	-	330	
Y218_HUMAN	SS	-	-	-	A	W	B	A	R	E	A	L	R	Q	I	P	L	E	R	I	I	V	E	T	D	A	P	Y	F	L	P	713

Figure 11(A)

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10      20      30      40      50      60
ATCTGGCTGGGTGCCACCAGATACCAACGTTGAAGAGTTCGAATTTGCCATTGGTACGG

70      80      90      100     110     120
TCGTGAACCTATCTTTGAGAAACCGCTGCCCGAAATTTGGTTTGGACATGTACTGTTAA

130     140     150     160     170     180
ATCTGTTTAATACGGCGCTGGCTTCAATATGGAAGTCCAGCCGCAACTGCTGTACTCC

190     200     210     220     230     240
AGAAAACCGTCTCTACCTCGAAGGGGTAGGACGCCAGCTTTATCCCAACTCGATTAT

250     260     270     280     290     300
GGAAAACGGCGAAGCGTTTCTCGAGTGGTGGATTAAAGATCAGGTGGTATTCTCGCCG

310     320     330     340     350     360
TGGTGACAGCAATTAAAGAAAAGCGCGTTCTGGGTGAAAAAATGCCAAGTCCCTG

370     380     390     400     410     420
AATTGCTTTACGACAGTTTGGCGCAGGGCAAGTATTTACAGCACAGTGTGATAAGATTG

430     440     450     460     470     480
CCCGGAGCTTCAGTCAATCATGTACGTCAGGCACAATCGCGTTATTTCTCGGAATTG

490     500     510     520     530     540
CCGCTACGTTAGTATTAAAGTGGCACATTTCTGTTGGTCAGCCACCTGAATGGGGGCTGA

550     560     570     580     590     600
TGGCCGGCTGGTTAATGGCAAGCTGGTCTGATCGCTGGTTTGTGGTTGGCGCAAAACAC

610     620     630     640     650     660
GCTGATTTTTCATCGCTCAAGCGCGGCGCTGTAACGTATAATGGCGCTTTGTTTAATCA
H R L C L I>

670     680     690     700     710     720
TCAICTACCACAGAGGAACATGTATGGGTGGIATCAGTATTGGCAGTTATGATTATTG
I I I H R G T C M C C I S I W Q L L I I>

730     740     750     760     770     780
CCGTCATCGTTGTACTGCTTTTGGCGCAAAAAGCTGGGTCCATCGGTTCGGATCTTG
A V I V V L L F G T K K L G S I G S D I>

790     800     810     820     830     840
GTGGTCCATCAAAGGCTTTAAAAAGCAATGAGCGATCATGAACCAAGCAGGATAAAA
G A S I K G F E K A M S D D E P K Q D K>

850     860     870     880     890     900
CCAGTCAGGATGCTGATTTTACTGCGAAAACATCGCGGATAAGCAGGCGGATACGAATC
T S Q D A D F T A K T I A D K Q A D T N>

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Figure 11(B)

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      910      920      930      940      950      960
AGGAACAGGCTAAACAGAGAGCGCGAGCGCCACGATAAAGAGCAGGTGTAATCCGTGT
Q E Q A K T E D A K R H D K E Q V>      V>
>
      970      980      990      1000     1010     1020
TIGATATCGGTTTITAGCGAAGTGTATTTGGTGTTCATCATCGGCTCGTCTGTTCTCGGCG
F D I G F S E L L L V F I I G L V V L G>
>
     1030     1040     1050     1060     1070     1080
CGCAACGACTGCGCTGTGGCGGTAAAAACCGTAGCGGGCTGGATTCCGCGGTTCGCTTCAC
P Q R L P V A V K T V A G W I R A L R S>
>
     1090     1100     1110     1120     1130     1140
TGGCCACAACCGTTCAGAACGAACTGACCCAGGAGTTAAACTCCAGGAGTTTCAGGACA
L A T T V Q N E L T Q E L K L Q E F Q D>
>
     1150     1160     1170     1180     1190     1200
GTCTGAAAAAGGTTGAAAAAGGCGAGCGCTCACTAACCTGACGCCGGAAGTCAAGCGTCCA
S L K K V E K A S L T N L T P E L K A S>
>
     1210     1220     1230     1240     1250     1260
TGGATCAACTACGCCAGCGCGCGGCTGATGAAGCGTTCCTACGTTGCAACCATCCTG
M D E L R Q A A E S H K R S Y V A N D P>
>
     1270     1280     1290     1300     1310     1320
AAAAGGCGAGCGATGAAGCGCACCATCCATAACCGGTGGTGAAGATAATGAAGCTG
E K A S D E A H I I H N P V V K D N E A>
>
     1330     1340     1350     1360     1370     1380
CGCATGAGGGCGTAACGCTTCCGCTGACAAACGAGGCCAGTTCCGCGGACAGAGC
A H E G V T P A A A Q T Q A S S F E Q E>
>
     1390     1400     1410     1420     1430     1440
CAGAAACCAAGCGAGAGCGGTTGTAACCTGCTGCGACGCTGACCGAAGAAACCGCTG
P E T T P E P V V K F A A D A E F K T A>
>
     1450     1460     1470     1480     1490     1500
CACCTTCCCTTCGTCGAGTGATAAACCGTAACATGTCTGTAGAGTACTCAACCGCT
      M S V E D I Q P L>
>
A P S P S S S D K P>
>
     1510     1520     1530     1540     1550     1560
TATACCGCATCTGATGAGCTGGTAAGCGTCTGCTGAACTGCATTATCGCGGTGATCGT
I T H L I E L R K R L L W C T I A V I V>
>

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Figure 11(C)

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Figure 11(D)

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2230      2240      2250      2260      2270      2280
TGAAGCAGAAAGCGAAAAAAGCTGAAGATATAATTCACCGCCCGTCAGGGCGGTTGTCAT
E A E S E K T E E>

2290      2300      2310      2320      2330      2340
ATGGAGTACAGGATGTTTGATATCGGCGTTAATTIGACCAGITCGCAATTTCGGAAGAC
M E Y R M F D I G V N L T S S Q P A K D>

2350      2360      2370      2380      2390      2400
CGTGATGATGTTGTAGCGTGGCGTTTIGACGGGGAGTTAATGGCTACTCAACCGCC
R D D V V A C A F D A C V N G L L I T G>

2410      2420      2430      2440      2450      2460
ACTAACCTGCGTGAAGCCACCGCGCAAAAGCTGGCGCGTCAGTATTGCTGCTGTTGG
T N L R E S Q Q A Q K L A R Q Y S S C W>

2470      2480      2490      2500      2510      2520
TCAACGGCGGGCGTACATCCCTCACGACAGCAGCCAGTGGCAAGCTGGGACTGAAGAAAGCG
S T A C V H F H D S S Q W Q A A T E E A>

2530      2540      2550      2560      2570      2580
ATTATTGAGCTGGCCGCGCAGCCAGAAAGTGGTGGCGATTGGTGAATGCTGCTCGACTTT
I I E L A A Q P E V V A I G E C G L D F>

2590      2600      2610      2620      2630      2640
AACCGCAACITTTTCGACGCGCGGAAGAGCAGGAGCGCGCTTTTGTGCGCCAGCTACGCATT
N R N F S T P E E Q E R A F V A Q L R I>

2650      2660      2670      2680      2690      2700
GCCGCAGATTTAACATGCCCGTATTATGCACTGTCCCGATGCCACGACCGGTTTATG
A A D L N M P V F M R C R D A R E R F M>

2710      2720      2730      2740      2750      2760
ACATTGCTGGAGCCCTGCGTGGATTAAGTGGCTGGTGGGTTCTTCATTGCTTTACCGGC
T L L E P M L D K L P C A V L H C F T G>

2770      2780      2790      2800      2810      2820
ACACGCCAAGAGATGCACCGGTGGTGGCCCATGGAAATTATATCGGCATTACCGGTTGG
T R E E M Q A C V A H G I Y I G I T G W>

2830      2840      2850      2860      2870      2880
GTTTGGGATGAAGACCGCGACTGGAGCTGCCCGAATTTTCCGTTGATTCCGCGGGA
V C D E R R G L E L R E L L P L I P A E>
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20

2690	2900	2910	2920	2930	2940
AAATTA	CTGATCG	AACTGAT	CGCCG	TATCTC	CTCCCTCGCG
ATCTAC	GCAGCA	AGCCAT	CTACGC	CAACG	CAAGCCA
K	L	L	I	E	T
D	A	F	Y	L	L
F	R	D	L	T	P
K	P				
					>
2950	2960	2970	2980	2990	3000
TCATC	CCCCGG	CGGCA	ACCA	CCGAC	CCCGC
ATCTG	CCCCC	ATATTT	TGGCA	CGTAT	TGCCCAT
TGG					
S	S	R	R	N	E
F	A	H	L	P	H
I	L	Q	R	I	A
H	M				
					>
3010	3020	3030	3040	3050	3060
CGTGG	AGAGAT	GCCCG	ATGG	CTGG	CCACCG
ATGCT	TAATG	CCCAAA	ACACT	GTGTT	
R	G	E	D	A	A
W	L	A	A	T	I
D	A	N	A	K	T
L	F				
					>
3070	3080	3090	3100	3110	3120
GCGAT	TGCG	TTTAC	AGTTT	GCGA	ACCTG
CTGCT	TATCT	TCAC	ACTG	TGCT	TAA
TCT	TTA	TCT	TTA		
G	I	A	F		
					>

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